

9598-066

SHEET 1 OF 16)

ACGTTGACAC	AGGAATGAAG	AGTGTATTGG	CTGAATCTTC	AAGCAGAGGC	GATATTGACC	60
ATGTGCTTTT	TAAATTGGCC	TGCGTGACCC	GCCCACTTGG	TGTAAAAGAA	GAACCGGCCA	120
AAGGGAGGGC	CTGAAGGACC	TCCACAGGAG	TGTGAGCAGC	ACTGCTTCAG	CAACAAAGCC	180
TCAGGTCCAC	ATCTTGGGAA	GAAT ATG	GCC ACT	TCC TGG	GGG GCT	231
		Met	Ala	Thr	Ser Trp Gly Ala Val Phe	
		1			5	
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG	279					
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln						
10 15 20 25						
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT	327					
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn						
30 35 40						
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT	375					
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr						
45 50 55						
GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG	423					
Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln						
60 65 70						
CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT	471					
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu						
75 80 85						
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG	519					
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu						
90 95 100 105						
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG	567					
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg						
110 115 120						
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG	615					
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu						
125 130 135						
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT	663					
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn						
140 145 150						
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC	711					
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser						
155 160 165						
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG	759					
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln						
170 175 180 185						
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT	807					
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly						
190 195 200						
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA	855					
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu						
205 210 215						
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT	903					
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr						
220 225 230						

Fig. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

(SHEET 3 OF 16)

TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAAATAGCTC	TAACCACTTG	TGGGGTGCAT	GGCTGGGACC	AGACTGTAAA	TC1TTTGGGA	1749
TTCTTTTGTC	AGAGTCTCTG	AAAGGAAAAA	AGAGAAAAAG	TTTGGAACTC	CATGCTAGAT	1809
TGCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAT	CTCGTTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTCG	TTATAAGCTG	ATTATCTGAA	ATCCCATTAAC	1929
CCATCAATGC	TGTTAAATTT	TTTCTTCTCA	CCCTTAATAC	ATTCCCTACC	CTAAAGAGCCT	1989
GGGGGAAATA	CCTGTTTTTG	CTTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GATTAGTAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATTT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

FIG. 1 (cont'd.)

[illegible]

```

peaNTase 1 ----MELLNNDTFLDTSMPAITSQYHONNULTSRCTFKGDSIASVAVPDAGSTGSR
potapyrase 1 MLNQNSHFPIFLANFLVLBSLLSKNVNAQPPRRRLSHSE . . . VAVPDAGSTGSR
mNTase 1 KATSWGATFMCTACVGGSTVYFRQOTWFEGYFLSNCCTINVSAGTFVAVPDAGSTGSR
yGDPase 1 KTPKHIATLMPNDEPGYLQDXTKTEQRYPELADAKSQTSTCSSENNVYVAVPDAGSTGSR

peaNTase 57 HEVYEPNOMDGLHIGKOVETTKITPGLSSYANNGEOAKSLIFLLEQAEADVVDLQCP
59 VHVPRFDEKSLAPICNNIBYFMATEPGLSSYADPKAAANSLPFLHCAEGVVPQNLQS
59 VHVPRFDEKSLAPICNNIBYFMATEPGLSSYADPKAAANSLPFLHCAEGVVPQNLQS
mNTase 61 KHVHCTVONTACQLPFGEGPSPDLYKPGLSAVVHQKQQAETVQELLEAVKDSIPRSHWE
61 YHEKRDVCTG . . . PPTLLDRAFDHLEPGLSSSDTDSVGAANSLPFLHCAEGVVPQNLQS
yGDPase 61 YHEKRDVCTG . . . PPTLLDRAFDHLEPGLSSSDTDSVGAANSLPFLHCAEGVVPQNLQS

peaNTase 117 KTFVRLGATAGLRLLNGDASEKILQSVRDCLSNRSTF . NUGPDVAVSINDCTOEGSYLWVT
119 ETEFLGATAGLRLLKCDAAEKILOAVRNATKRNOSTF . HSKDQWVTHLDCTOEGSYLWVT
121 ETEFLGATAGLRLLPEQKAGALILEVEETPKN . SPP . TVPBCVVSINDCTOEGSYLWVT
mNTase 119 CTEVAKKATAGLRLLCDAKSKILSAVRDHEKDYFP . TVPBCVVSINDCTOEGSYLWVT
yGDPase 119 CTEVAKKATAGLRLLCDAKSKILSAVRDHEKDYFP . TVPBCVVSINDCTOEGSYLWVT

peaNTase 176 VNVALGNLGRKRTK . . . TVGVIDLGGGSVQMAAYAVSKKTAKNAPKVLADQDLPYKKVYVKG
178 INYLLGNLGRKRTK . . . TVGVIDLGGGSVQMAAYAVSKKTAKNAPKVLADQDLPYKKVYVKG
179 VNVALGNLGRKRTK . . . TVGVIDLGGGSVQMAAYAVSKKTAKNAPKVLADQDLPYKKVYVKG
mNTase 179 VNVALGNLGRKRTK . . . TVGVIDLGGGSVQMAAYAVSKKTAKNAPKVLADQDLPYKKVYVKG
yGDPase 179 VNVALGNLGRKRTK . . . TVGVIDLGGGSVQMAAYAVSKKTAKNAPKVLADQDLPYKKVYVKG

peaNTase 234 IPVCLVHSYLSGCRPSRAEILKL . . . . . PRSPNFCILAGNCGV
236 KLVCLVHSYLSGCRPSRAEILKL . . . . . PRSPNFCILAGNCGV
238 STEKLYTHSYLGFGKAAALATLGA . . . . . PRSPNFCILAGNCGV
mNTase 238 STEKLYTHSYLGFGKAAALATLGA . . . . . PRSPNFCILAGNCGV
yGDPase 238 STEKLYTHSYLGFGKAAALATLGA . . . . . PRSPNFCILAGNCGV

peaNTase 276 TNSGCEPKATAYTSGN . . . . . NNNKCNNTIRNALKMYPYPCYCNCEGGMNNGCCGN . . .
278 SYGGYDYKVKAPKKG . . . . . SWKRCRRTTRHAKKINAKM . . . . . ECTNCGVNNNGCCGN . . .
280 KCEPRWLEENIFGCV . . . . . KYTYGGNQGEGMGFEPCYAEVLRVQCKDHQPEEVR . . .
mNTase 280 KCEPRWLEENIFGCV . . . . . KYTYGGNQGEGMGFEPCYAEVLRVQCKDHQPEEVR . . .
yGDPase 280 KCEPRWLEENIFGCV . . . . . KYTYGGNQGEGMGFEPCYAEVLRVQCKDHQPEEVR . . .

peaNTase 328 GGRNTPASSSSNYLPEETCHVDKSPFNFDPRVDIEKAKEACALNFEAKSTYFLLKK
330 GGRNTPASSSSNYLPEETCHVDKSPFNFDPRVDIEKAKEACALNFEAKSTYFLLKK
332 GGRNTPASSSSNYLPEETCHVDKSPFNFDPRVDIEKAKEACALNFEAKSTYFLLKK
mNTase 332 GGRNTPASSSSNYLPEETCHVDKSPFNFDPRVDIEKAKEACALNFEAKSTYFLLKK
yGDPase 332 GGRNTPASSSSNYLPEETCHVDKSPFNFDPRVDIEKAKEACALNFEAKSTYFLLKK

peaNTase 388 NYASYVCMDDLYQYVLLVDGFGLDLQXITGKEIEYQDAIVFAAWPFCNVYASALPK
390 NYASYVCMDDLYQYVLLVDGFGLDLQXITGKEIEYQDAIVFAAWPFCNVYASALPK
392 NYASYVCMDDLYQYVLLVDGFGLDLQXITGKEIEYQDAIVFAAWPFCNVYASALPK
mNTase 392 NYASYVCMDDLYQYVLLVDGFGLDLQXITGKEIEYQDAIVFAAWPFCNVYASALPK
yGDPase 392 NYASYVCMDDLYQYVLLVDGFGLDLQXITGKEIEYQDAIVFAAWPFCNVYASALPK

peaNTase 448 FERUNYFV-----
450 FERUNYFV-----
452 FERUNYFV-----
mNTase 450 FERUNYFV-----
yGDPase 450 FERUNYFV-----

```

FIG. 2

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

9598-066

(SHEET 6 OF 16)

GTGGGGTCGT ATCCCGCGGG TGGAGGCCCG GGTGGCGCCG GCCGGGGCCG GGGAGCCCAA 60
 AAGACCGGCT GCCGCCTGCT CCCCGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC 120
 GCGCGGTGCA TGGAAATGGGC TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA 180
 AAAACGAGCT ACATTTTTC A GCAGCCGCAG CACGGTCCTT GGCAAACAAG G ATG AGA 237
 Met Arg
 1

AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC 285
 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
 5 10 15

CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG 333
 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
 20 25 30

CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC 381
 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
 35 40 45 50

CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT 429
 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
 55 60 65

GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC 477
 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
 70 75 80

ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA 525
 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
 85 90 95

ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT 573
 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
 100 105 110

TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA 621
 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
 115 120 125 130

CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC 669
 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
 135 140 145

ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA 717
 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
 150 155 160

GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA 765
 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
 165 170 175

TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA 813
 Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
 180 185 190

GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC 861
 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
 195 200 205 210

TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA 909
 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
 215 220 225

FIG. 4

GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCTC CTGTCCTGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC TGGCATCAGC CTCTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC	1697 1757 1817

FIG. 4 (cont'd.)

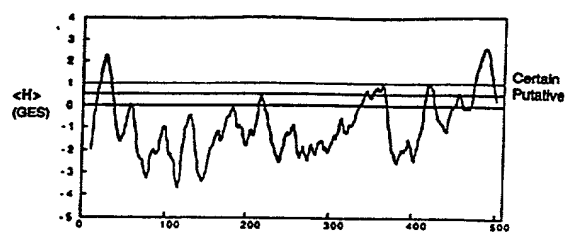
[illegible]

(HEET 8 OF 16)

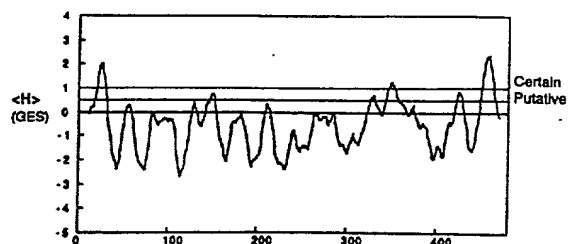
AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAACC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGCTC	GCGGGGCTGT	1937
GGCTGCTGGT	GTGCTGATCC	CTGCGATGGG	AGCTTTGTCT	CCCAGCTGTG	CAGTTTCTCT	1997
CCCAGGGCAG	AGCTCCCCTT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCTTGCGTG	2057
CTCTGGGGAA	CGCGAGGGAC	AGCCATAACA	CCCCCGGAGC	AGTAGGTTGT	GGCGGCACCA	2117
CTGGGAACTG	TGGACTTGAG	TGTGTTTTCT	TCTCTTGGG	TATGAATTGT	TGAGTTCACC	2177
CAGAGGCCGT	GCTCTCTCAC	ACATTGTGTG	GTTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGGC	2297
ATGAGCTGCT	GTAACCTATT	TGTGGCTGTG	TGCTTGAGT	GACGCTCTGT	TCGTGTGGGT	2357
GCCAAAGTGT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GCGCAGCTGA	GCCACAGTCC	GACAACCAAG	CTCTCGTGT	CTCGGGCCAG	2537
CATCCGCCCA	CCTCGGGCTG	ACCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTGGG	GCTGAGCCCC	TTAGAGTGCT	TCAGTGAATG	2657
TACAGTGCCT	GGCACGAGCT	GAACTCATG	GTTTCACTC	CCAATAAAG	GTTGACAGGG	2717
GCTTCTCCTT	CAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA		2762

FIG. 4 (cont'd)

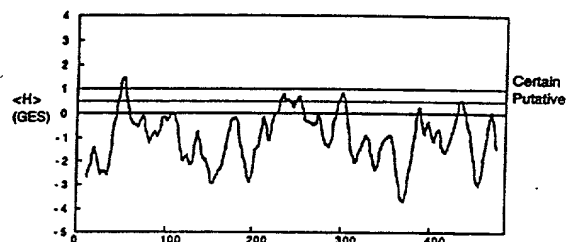
CD39



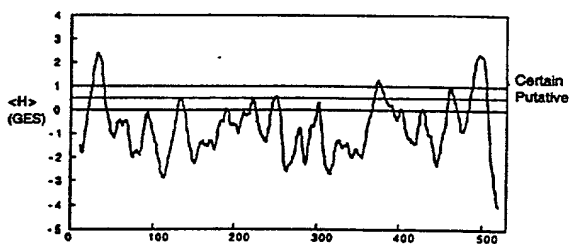
CD39L1



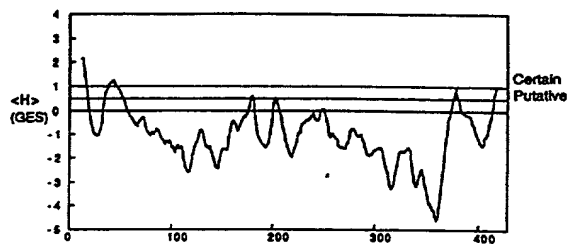
CD39L2



CD39L3



CD39L4



Amino acid position

FIG. 5

9598-066

SHEET 10 OF 16)

ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG	60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT	112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys	
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC	160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC	208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT	256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA	304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165 170	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	

Fig. 6

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	
235 240 245 250	
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	
255 260 265	
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	
365 370 375	
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser	
380 385 390	
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC	1312
Thr Trp Asn Phe Cys Glu Asn Trp Ser Gln Leu Pro Leu Leu Leu	
395 400 405 410	
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn	
415 420 425	
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr	
430 435 440	
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala	
445 450 455	
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA	1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	
460 465 470	
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	
475 480 485 490	

FIG. 6 (cont'd.)

CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC	1703
Asp His Ala Val Asp Ser Asp	
525	
TGCTTAGAGT CAGCCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTCAGGAAA	1763
TACAACTAAC TAAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC	1823
AGCACCTCTT GAGGCATCCC TTGGCTATTC TGTGCATATT GTTCTTCAGA GACCTCACTA	1883
CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA	1943
TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATTG	2003
ACCTCAGGGC TCAGTTTCCA TTTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA	2063
AGCATTTCGC CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT	2123
TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAATAT AGTATCTGGG	2183
GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA	2243
TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG	2303
GAATTCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGTG ATCATCTCTCA	2363
TCTCACCATT GTATTGCTAT GCCCTCCAT AAAACACAT TGATCCCTAG CAAGATTATT	2423
GCATTCCAGA TTTTACTGCC TTTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTTCCATT	2483
GTATCATGG TGTATATATT TTTGTACCA TTCCACACAG TATACTTGAT GTTGTATAG	2543
AACGAACATC CTAATCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT	2603
GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC	2663
TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA	2723
TTATTTTCATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTTGA	2783
AAAAAAAAAA AAAA	2797

FIG. 6 (cont'd)

GCGCGCGCGT TTTCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC 60
 TCATACAGAC AAGATCATT TGGTGTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTTG 120
 AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTCAGA AGGAAAGAAA AAATTGCCTC 180
 TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAGCCT CCACCCAGCC ACATCTGGG 240
 AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA 288
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
 1 5 10

TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT 336
 Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
 15 20 25 30

GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC 384
 Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
 35 40 45

ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT 432
 Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
 50 55 60

CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA 480
 His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
 65 70 75

GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA 528
 Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val
 80 85 90

GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG 576
 Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val
 95 100 105 110

GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC 624
 Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val
 115 120 125

CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG 672
 Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu His Lys Ala Lys
 130 135 140

GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG 720
 Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu
 145 150 155

GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA 768
 Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile
 160 165 170

TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC 816
 Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His
 175 180 185 190

AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA 864
 Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln
 195 200 205

ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG 912
 Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg
 210 215 220

GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT 960
 Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr
 225 230 235

Fig. 7

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Arg Leu Ala Thr	
240 245 250	
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	
255 260 265 270	
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	
275 280 285	
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Val Gly Glu Pro	
290 295 300	
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	
305 310 315	
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	
320 325 330	
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	
335 340 345 350	
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG	1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu	
355 360 365	
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC	1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr	
370 375 380	
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC	1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385 390 395	
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400 405 410	
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC	1539
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415 420 425	
GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG	1599
TTTCTGAAC AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT	1659
TACACATCTA ATGTGAAC TGCTTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA	1719
TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTTAACCTTG GAGTGAGAGC	1779
CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATTT CAACCCTTG AGTGCCTCAT	1839
TCCACTGAAT ATTAAATTT TCCTCTTAAA TGGTAACTG ACTTATTGCA ATCCCAAGAC	1899
CCATCAATAT CAGTATTTTT TTCCTCCCTA TACAGTGCCC TGCCACCCT TATCTGCACC	1959
CACCTCCCCT GAAAAAGAGA GAAAAAATA AAAAAAATA	1998

Fig. 7 (cont'd.)

ACR I

ACR II

ACR II

ACR III

ACR IV

```
CD39L2      485 -----  
CD39L4      422 -----  
CD39L1      439 GKKKQFSSHWVDELLRGGGLLAALGHHGRGVHSLPLSTI-----  
CD39L3      476 ELRLPPPVSVOTLAPFGAALLCAAFADATCSGAKRKRSZHAFADEAVDSD  
CD39        468 LSTPHSHSSEVDFGFLPSIVLRVALGDLLEPKPPTFWDKM-----
```

Fig. 8

[illegible]

peaGDP 1 -----
 potapyrase 1 -----
 CD39L2 1 MKKGIRYTSRKTSYIFQQPQGPNQTRM K E H H G S L R V A V Y P L G L C V Y F Y Y
 CD39L4 1 -----
 dNTPase 1 ----- MKYET L T D E K F P R R S G S F N A S S G O N R P S G
 yGDPase 1 ----- K P E

ACR I

peaGDP 2 K L L K L I T F S F S I I S O I L S N H L T S R K I F E E I S S Y A F D A G S T G S R H V V
 potapyrase 6 S H I F T I L F L V L P L S L L S K H V N A O I P E R R E L L S E S E . . . Y A F D A G S T G S R V H V
 CD39L2 61 M H R A T A D Q A F S T R P G A R A G O A K S P L A A G H E V F Y I H F D A G S T G R V H V
 CD39L4 7 T E F L A V C V C S A V H R N Q S T F E C I L S S C P S V S A S T L Y I H F D A G S T G R H V V
 dNTPase 37 K I S F L C I I S V I L L G F V F G V S E N A S P L I R L S K F G Y S K Q V A L I D A G S T G S R V L A V
 yGDPase 5 D S L I P H D R P G T L Q D S K L O N Y P E L A D A K S Q S Q T C S E E R S Y V I L I D A G S T G S R V H V

ACR II

peaGDP 61 E F N O M C D L L R I S K G E Y K T P G L S S Y A P E O A A K S L I P L L Q A E D V V E D D F Q P K T P V
 potapyrase 63 E H K I G L L P I C N M E Y P A T E P G L S S Y A D P K A A A N S L P L I D C A G V U V Q L O S E T P E
 CD39L2 119 Q S T E P E R R E T S T T H S T P K A V K P O L S Y A D D V E K A T C R L L I D V A R Q D P F C F K A I P E
 CD39L4 96 T F V O R E C Q L I L E C E V P D V K P O L S V D Q P K O A E C G L L V A N D S P S S E K A T P V
 dNTPase 66 K P R S F I D N K L V I T L P K E R K P O L S S A D E A L A S K I L L D E A N A F P E H S S T P E
 yGDPase 65 K E T . . . C T S P E T L L D E K F E M E P G L S S P D T D S V C A A N S L P L L K V A M Y V I K A S C T P V

ACR II ACR III

peaGDP 121 R E C A T A G L R L L G D A E K I L Q V R D L E N S T F M V P D A V S I D G T O C G S Y L L V T V N V A
 potapyrase 123 E C A T A G L R L L G D A E K I L O A V R L V N S T F K S F D O M V I D G T O C G S Y L L V T V N V A
 CD39L2 178 V L K A T A G L R L L F G K A K L O R V E E A S P F E V G D D C Y S I C T D E C G V A R T L L
 CD39L4 126 V L K A T A G L R L L P E K A K I L E V A S P F E V K G V S I M C D D E L A N V T V N L
 dNTPase 156 V L K A T A G L R L L P S K A E I L A V R D L E A K S E F E V K M D A V E I M C T D E C S V T V N L
 yGDPase 123 A K K A T A G L R L L G D A E S K I L S A V R D E L K D Y P F E V G D V S I M C D E G V A R T V N L

ACR IV

peaGDP 180 L G N L G K M Y T K . . . V G V D L G G G S V C A A V S K K T A K N A P L V A D G D P Y K K V I L K G I P R
 potapyrase 182 L G N L G D M Y K S . . . T T D L G G G S V C A A S M E Q F A K A P O M E D G S P Y S K K H S K D V N
 CD39L2 236 T C S E K T P G G S . . . V G D L G G G S T C I A F L P E V E G . . . T A S F F G Y L T A R E K Y T K
 CD39L4 184 T C S E K H R O E . . . V G T L D L G G S T C I A F L P O E K . . . T E Q T P R G I L T S F E N S K Y K
 dNTPase 214 L G R S E T M O . . . A . . . D L G G G S T C I A F L P D F D . . . S V P V T K Y E R V U T S S K I N
 yGDPase 183 L G N I G A N G K L P A A V F D L G G G S T C I V F E R E F F I N E K M V . . . D G E H K F K K F G E R N T

ACR V

peaGDP 238 J Y V H S Y L G F G R A P R A C I L L T F S E M P C L L A S P H G Y
 potapyrase 239 J Y V H S Y L M G O A R A C I P R A S R N E S M P C A E S C C G Y
 CD39L2 289 J Y V H S Y L G L R A P L A I L G T E G R P K D G R E V S P C I S E S P K E
 CD39L4 237 J Y T H S Y L G F G L R A P L A T L C A L E T S T O C H T F S S A C I P R W L L E
 dNTPase 264 J Y T H S Y L G L R A P R A T T H G Y K N D T L E S V C H E B I T A N A T N
 yGDPase 238 J Y Q T S E L G G U K I F R N A S V I V E N A L K O K L L G D N T K T H Q L S E C P K E V T I N E K T

peaGDP 276 T Y G C E K N A I T T G . . . M E R K E N T I R A L K L N T F C P I O N C T F C G W N G G . . . S G M G O K N
 potapyrase 277 T Y G C V D M Y K P M C S E W K R S R L T R A L K T H A C C E E C T F N G V W H G G . . . S G D G O K N
 CD39L2 335 E H E V T R N S G A N A S L E S L C A R S E I C O H R V H R T E L K H V
 CD39L4 282 I G G V K Y Q T G C Q E C E V G S E P I A N V L T V R G K L E E V Q R G S
 dNTPase 308 T Y G N V O R V S G K E M S S A G O P I V D E D A C E L V K S K V M P L K K P F T K O H A
 yGDPase 298 L E S K E T Y T D F I G F D P S G A D C H F L I D E L N K A C C S P F C S P H G V H P S L V T F K S N A

peaGDP 332 T A G S S F Y L P D T G H V D A S T E T L E P V D I E T R A N E A C A L H F E A R S P P L E K H V S
 potapyrase 333 I H A G S F Y E I A Q V C V D K F S S A R P I O N L M A R V A C Q T N V I D I K S T P K T O H I
 CD39L2 379 F Y A F S Y Y D L A A G V S E D A E K G G S L V V C D E I A A I V C R T L E T P S S P
 CD39L4 326 F Y A F S Y Y D R A V O T D E D I E K G G I L K V E D E K A E V C D N L E F T S C S P
 dNTPase 360 F A F S Y R A I E T G V E P L A S G E T T V S A W R K A C E I C A I F E D E Q P
 yGDPase 358 I V G S Y F Y D R A T L C E F L F L M E N D A R I V C R E E W H E V E N G I A C H L D E L E S D S

peaGDP 392 C H D L I Y Q Y V L L V D G F G L P L O K I T S K I I Y O A V E A A W P L C M A V A S L P R F E R N
 potapyrase 392 C H D L I Y I F L L V D G F G L H P E K E I I D H O I K Y V G A A W P L C C A I D S S T T N K I R N
 CD39L2 428 P E C H D L I Y S L L C L G F P R S E V N L T K I D E V E E N A L C A I P H Y D S I M Q S F
 CD39L4 378 P L C H D L E Y L L D C G C T A D T V S O U T R E K N E E E N A L C A I P H Y D S I M Q S F
 dNTPase 406 P E C F D L E I S T L R C G L L H O C K I L I R K I D G H E I E N A L C A I P H Y D S I M Q S F
 yGDPase 415 H F C D L E O V E L L E T S C D P L O E E T S K T I A N N E T A C C A G A F L R K D H W K C M

peaGDP 452 M Y F V
 potapyrase 452 A S H
 CD39L2 483 A S
 CD39L4 429 ----
 dNTPase 462 ----
 yGDPase 471 Q S H

FIG. 9